



SEQUENCE LISTING

<110> YISSUM Research Development Company of the Hebrew
YARKONI, Shai
NECHUSHTAN, Amotz
LORBERBOUM-GALSKI, Haya
MARIANOVSKI, Irina

<120> CHIMERIC TOXINS FOR TARGETED THERAPY

<130> 1268-073

<140> 09/147,346

<141> 1998-12-04

<150> PCT\IL97\00180

<151> 1996-06-04

<160> 4

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Escherichia coli

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Gln Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro
35 40 45

Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu
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Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln
65 70 75 80

Val Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly
85 90 95

Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu
100 105 110

Ala Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp
115 120 125

Glu Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val
130 135 140

Ala Ala Gly Ala Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu
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Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp
165 170 175

Val Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu
180 185 190

Leu Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly
195 200 205

Tyr His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly

19

210 215 220
 Val Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr
 225 230 235 240
 Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu
 245 250 255
 Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr
 260 265 270
 Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu
 275 280 285
 Ala Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro
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 Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly
 305 310 315 320
 Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val
 325 330 335
 Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu
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 Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro
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20

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 35 40 45
 Gln Gly Val Leu His Tyr Ser Met Val Leu Glu Gly Gly Asn Asp Ala
 50 55 60
 Leu Glu Leu Ala Ile Asp Asn Ala Leu Ser Ile Thr Ser Asp Gly Leu
 65 70 75 80
 Thr Ile Arg Leu Glu Gly Gly Val Glu Pro Asn Lys Pro Leu Arg Tyr
 85 90 95

21

Ser Tyr Thr Arg Gln Ala Arg Gly Arg Trp Ser Leu Asn Trp Leu Val
100 105 110

Pro Ile Gly His Glu Lys Pro Ser Asn Ile Lys Val Phe Ile His Glu
115 120 125

Leu Asn Ala Gly Asn Gln Leu Ser His Met Ser Pro Ile Tyr Thr Ile
130 135 140

Glu Met Gly Asp Glu Leu Leu Ala Lys Leu Ala Arg Asp Ala Thr Phe
145 150 155 160

Phe Val Arg Ala His Glu Ser Asn Glu Met Gln Pro Thr Leu Ala Ile
165 170 175

Ser His Ala Gly Val Ser Val Val Met Ala Gln Thr Gln Pro Arg Arg
180 185 190

Glu Lys Arg Trp Ser Glu Trp Ala Ser Gly Lys Val Leu Cys Leu Leu
195 200 205

Asp Pro Leu Asp Gly Val Tyr Asn Tyr Leu Ala Gln Gln Arg Cys Asn
210 215 220

Leu Asp Asp Thr Trp Glu Gly Lys Ile Tyr Arg Val Leu Ala Gly Asn
225 230 235 240

Pro Ala Lys His Asp Leu Asp Ile Lys Pro Thr Val Ile Ser Glu Glu
245 250 255

Leu Glu Phe Pro Glu Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln
260 265 270

Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg
275 280 285

Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val
290 295 300

Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val
305 310 315 320

Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu
325 330 335

Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala
340 345 350

32

Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu
355 360 365

Ala Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala
370 375 380

Ala Gly Glu Cys Ala Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu
385 390 395 400

Ala Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val
405 410 415

Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu
420 425 430

Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr
435 440 445

His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val
450 455 460

Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile
465 470 475 480

Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro
485 490 495

Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val
500 505 510

Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala
515 520 525

Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu
530 535 540

Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg
545 550 555 560

Leu Glu Thr Ile Leu Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile
565 570 575

Pro Ser Ala Ile Pro Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp
580 585 590

Pro Ser Ser Ile Pro Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp
595 600 605

Tyr Ala Ser Gln Pro Gly Lys Pro Pro Arg Glu Asp Leu Lys
610 615 620

61

24
